

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 6, 2002, 23:33:11 : Search time 1527.5 Seconds
(without alignments)
16168.980 Million cell updates/sec

Title: US-10-025-514-7

Perfect score: 1525

Sequence: 1 tctagaccatgctgtgaaag.....ccaactcagaagtgcgac 1525

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: gb_gss:*

18: em_gss_hum:*

19: em_gss_inv:*

20: em_gss_pln:*

21: em_gss_vrt:*

22: em_gss_fun:*

23: em_gss_mam:*

24: em_gss_mus:*

25: em_gss_other:*

26: em_gss_pro:*

27: em_gss_rod:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	433.2	28.4	2478	11	AF130068
2	431.6	28.3	2571	11	AF113676
3	331.6	21.7	1392	11	AK002537
4	318.8	20.9	1296	11	AK004999
5	309.8	20.3	887	14	BO643710
6	305.4	20.0	907	14	BO648909

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7 289.6 19.0 895 14 BO653587
8 287 18.8 985 14 BM924019
9 285.2 18.7 982 14 BO646142
10 283.8 18.6 924 14 BO958958
11 274.8 18.0 1194 14 BM924813
12 273.4 17.9 907 14 BO650189
13 271.4 17.8 891 14 BO646948
14 270.4 17.7 959 14 BO648524
15 268 17.6 796 12 BO567260
16 264.8 17.4 833 14 BO007663
17 264.8 17.4 991 14 BO064738
18 263.8 17.3 917 14 BO650502
19 263.6 17.3 687 10 BO649258
20 263 17.2 916 14 BO644130
21 262 17.2 686 12 BO569467
22 261 17.1 1012 14 BO064473
23 260.2 17.1 977 14 BO654015
24 259.6 17.0 740 10 BO653778
25 259.6 17.0 944 14 BO645533
26 256 16.8 869 13 BI219058
27 254 16.7 917 14 BO650698
28 253 16.6 654 12 BG563537
29 251.4 16.5 884 12 BG536548
30 250.6 16.4 746 12 BG566873
31 250.2 16.4 745 9 A1114643
32 249.8 16.4 1044 9 A1528087
33 249.6 16.4 813 13 BI759000
34 249.4 16.4 764 12 BF384318
35 249 16.3 731 10 AV649144
36 248.8 16.3 804 12 BG618951
37 247.4 16.2 813 14 BO182052
38 245.8 16.1 780 9 A1110706
39 244.2 16.0 992 13 BI246204
40 243.8 16.0 752 12 BG618001
41 243.2 15.9 674 14 BM724546
42 243.2 15.9 759 12 BG533293
43 243 15.9 749 9 A1528727
44 242.8 15.9 790 13 BI761275
45 242.6 15.9 934 14 BO646994

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ALIGNMENTS

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LOCUS Homo sapiens clone FLB8226 PRO2209 mRNA, complete cds.
DEFINITION
ACCESSION AF130068
VERSION AF130068.1 GI:11493442
KEYWORDS HTC.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 2478)
Zhang,C., Yu,Y., Zhang,S., Wei,H., Bi,J., Zhou,G., Dong,C., Zai,Y.,
Xu,W., Gao,F., Liu,M. and He,F.
TITLE Functional prediction of the coding sequences of 75 new genes
deduced by analysis of cDNA clones from human fetal liver
JOURNAL Unpublished
REFERENCE
2 (bases 1 to 2478)
Zhang,C., Yu,Y., Zhang,S., Wei,H., Bi,J., Zhou,G., Dong,C., Zai,Y.,
Xu,W., Gao,F., Liu,M. and He,F.
TITLE Direct Submission
JOURNAL Submitted (23-FEB-1999) Department of Experimental Hematology,
Institute of Radiation Medicine, Beijing Taiping Road 27, Beijing,
Beijing 100850, P. R. China
FEATURES
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1. .2478
/organism="Homo sapiens"
/db xref="taxon.9606"
/clone="FLB8226"

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[illegible]

/tissue_type="hepatocellular carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library.

BASE COUNT	242 a	224 c	232 g	187 t	2 others
ORIGIN					
Query Match	20.3%	Score 309.8	DB 14	Length 887	
Best Local Similarity	60.0%	Pred. No. 3.1e-69			
Matches 532	Conservative 0	Mismatches 354	Indels 1	Gaps 1	
QY	519	GCATGTTGAGTTTAGTACTAAAGCCGATACCCATGACGAGATTTTGAAGGTTTAAAC	578		
Db	1	GCAATGCTCTCCCTGGGACCAAGGCTGACACTCAGATGAATCCTGGAGGCGCTGAAT	60		
QY	579	TTAATTTGACCGAATCCAGAACCCCAATTCACGAGGGTTTCAAGAGTTGTTGAGA	638		
Db	61	TTCAACCTCACGGAGATTCCGGAGGCTCAGATCCATGAAGGCTCCAGGAACCTCCCGT	120		
QY	639	ACTTTGAATCAACCTGATTTCAATTCGAATTACTACTGTAAGGTTTATTTTGTCT	698		
Db	121	ACCTCAACGACGACAGCAGCTCCAGCTGACCCAGCGCAATGGCTGCTTCTCAGC	180		
QY	699	GAAGGTTTAAATTTGGTTGACAAATTCCTAGAAGACGTCGAAGAACTATATCATAGTGAG	758		
Db	181	GAGGCGCTGAAGCTAGTGGTAAGTTTTTGGAGGATGTTAAAGCTGTACCACTCAGAA	240		
QY	759	GCTTTTACCGTTAATTTGGTGATCTACGAGAGCTAAAGCAAAATTAATGATATGTT	818		
Db	241	GCCTTCACTGTCACTTCGGGACACCCAGAGGCGCAAGAACAGATCAACGATACGTTG	300		
QY	819	GAGAAAGCCACCCAGGGTAAAGTACCTAGTTAAGAAATTAGATCGTGATACCGTC	878		
Db	301	GAGAGGGTACTCAAGGGAATTTGTGGATTGTGTCAGGAGCTTGACAGAGACACAGTT	360		
QY	879	TTCCGACATAGTTAACTATATTTTTCNAGGTTAAGTGGGAACGCTCTTCGAGGTTAAA	938		
Db	361	TTTGTCTGTGGTAATACATCTCTTTAAAGGCAATGGGAGAGACGCTTTGAAGTCAAG	420		
QY	939	GATACTGAAGGAGGAGATTTTCATGTTGATCAAGTTACTACTGTCGAAGTCCCATGATG	998		
Db	421	GACACCGAGGAAGAGGACTTCCAGCTGGACACAGGTGACCCGTTGAAGGTGCTATGATG	480		
QY	999	AAAGACTGGGTATGTTCAATATTCAACATTCGAAAAATTAAGTTCTTGGGTCTTATTA	1058		
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QY	1059	ATGAAGTATTTAGTAAAGCTACTGCTATTTTTTTTACGACGAGGATGAAGCTTCAA	1118		
Db	541	ATGAATACCTTGGGCAATGCGACCGCATCTTCTTCTGCTGATGAGGGAACACTACAG	600		
QY	1119	CATTTAGAGATAGTGTGACTCATGACATATTACTATAATTTTATAGAGAACGAGGATCGT	1178		
Db	601	CACCTGGAATATGAATCAACCCAGATATCATCACCAGTTTCTTGGAAAAATGAAGACAGA	660		
QY	1179	CGTAGCGCTCTCTGCACTGCTGCAAAAGTTAAGTATATCACCAGTACTTACGACTTAAATCT	1238		
Db	661	AGGCTGCCAGCTTACATTTTACCAGAACTGTCCATTACTGMACTTATGATCTGAAGAGC	720		
QY	1239	GTTTTAGCCAGTTAGTATTTACCAAGTTTCTTCTAACGGTCCGCAATTTGAGTGGTGT	1298		
Db	721	GTCCTGNGTCAACTGGGCACTACTAAGGTTCTTCAGCAATGGGCTGACCTCTCCGGNGTC	780		
QY	1299	ACTGAAGAAGCTCCATTTAAATTAAGTAAAGCTGTTTCCACAAAGCCGCTTAACTATGAT	1358		
Db	781	ACAGAGGAGGACCCCTCAAGCTCTCCAGGC-GTGCATTAAGGCTGTGCTGACCATCGAC	839		

QY	1359	GAAGAAGGTACCGAGCGCGCGCTATGTTCTCTGGAAGCTATTCC	1405		
Db	840	GAGAAAGGACTGAAGCTGCTGGGCGCATGTTTTAGAGCCATACC	886		
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BO648909					
LOCUS	BO648909	907 bp	mRNA	linear	EST 15-JUL-2002
DEFINITION	AGENCOURT_8351269 NIH_MGC_100 Homo sapiens cDNA clone IMAGE:6286839				
	5', mRNA sequence.				
ACCESSION	BO648909				
VERSION	BO648909.1	GI:21773081			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	1	(bases 1 to 907)			
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/				
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)				
JOURNAL	Unpublished (1999)				
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgabbs-r@mail.nih.gov Tissue Procurement: CGAP (Stanford) CDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LICM2488 row: e column: 16 High quality sequence stop: 721.				

FEATURES

source
1. .907
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/db_xref="taxon:9606"
/clone_lib="IMAGE:6286839"
/tissue_type="hepatocellular carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: liver; Vector: pOPB7; Site:1: XhoI; Site:2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."

BASE COUNT	246 a	228 c	239 g	192 t	2 others
ORIGIN					

Query Match 20.0%; Score 305.4; DB 14; Length 907;
Best Local Similarity 59.8%; Pred. No. 4.4e-68;
Matches 530; Conservative 0; Mismatches 356; Indels 1; Gaps 1;

QY	541	AGCCGATACCCATGACGAGATTTTGAAGGTTTAACTTATTTGACCGAAATCCCCAG	600		
Db	15	AGGCTGACACTCAGCATGAATCTCGAGGCGCTGAATTTCAACCTCAGCGAGATTCGG	74		
QY	601	AAGCCCAAAATTCAGGAGGTTTTCAGAGCTTGTGAGAACTTTGAATCAACCTGATTC	660		
Db	75	AGGCTCAGATCCATGAAGGCTTCCAGAACTCCTCGTACCCTCAACCCAGCAGACG	134		
QY	661	AATTCGAATTAAGTGTAAACCGTTTATTTTGTCTGAAGGTTTAAATTTGGTTGACA	720		
Db	135	AGCTCCAGCTGACCCAGCGCAATGGCTGTTCTCAGCGAGGCGCTGAAGCTAGTGATA	194		
QY	721	AATTCCTAGAAGAGCTCAAGAACTATATCATAGTAGGAGCTTTTACCGTTAAATTTGGTG	780		
Db	195	AGTTTTTGGAGGATGTTAAAGAGTTGTACCACTCAGAGGCTTCTACTGTCAACTTCGGGG	254		

Db 777 ACATCCAGCAGCTGTGAAGAGCTGTCCAGTGGGTGCTGCTGATGAATACCTGGGGCATG 836
 QY 1078 CTACTGCTATTTTATTTTACCAGAGGAGTAACTTCAACATTTAGAGAA 1129
 Db 837 CCACCGCCATCTCTTCTGCTGGATGAGGGAACACTACAGCACCTGGGAAA 888

RESULT 8
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 LOCUS AGENCOURT_6709923 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5760183
 DEFINITION 5', mRNA sequence.
 ACCESSION BM924019
 VERSION BM924019.1 GI:19374398
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 985)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: CLAM12806 row: m column: 16
 High quality sequence stop: 707.
 Location/Qualifiers
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 /db_xref="taxon:9606"
 /clone="IMAGE:5760183"
 /clone_lib="NIH_MGC_116"
 /lab_host="DH10B"
 /note="Organ: pooled colon, kidney, stomach; Vector:
 PCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
 source anonymous pool of 3 colons, age 26 yo male, 49 yo
 female, 71 yo male colon; 46 yo male kidney, and pool of 2
 stomachs, 62 yo male and 70 yo female. Library is
 oligo-dT primed and directionally cloned (EcoRV site is
 destroyed upon cloning). Average insert size 1.4 kb,
 insert size range 1-3 kb. Library is normalized and
 enriched for full-length clones and was constructed by
 Gruber (Invitrogen). Research Genetics tracking code
 023. Note: this is a NIH_MGC Library."
 258 a 270 c 242 g 213 t 2 Others

BASE COUNT 258 a 270 c 242 g 213 t 2 Others
 ORIGIN

Query Match 18.8%; Score 287; DB 14; Length 985;
 Best Local Similarity 59.5%; Pred. No. 2.6e-63;
 Matches 519; Conservative 0; Mismatches 351; Indels 2; Gaps 2;

QY 298 TGTGTGTGAAGTCTCTGTGTTCCCAAGTCAAGCCATGAAGCCCTCAAGCGGCGCG 357
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 QY 358 CTCAAAAACCGACACCATCATCAGCCAAAGACCATCCGACTTTTATAAAATTAATC 417
 Db 114 CCAGAAGACAGATACATCCACCATGATCAGATCACCCACCTCACAGATCACCC 173
 QY 418 CAAATTTAGCGAATTTGCTTTTCTTTCTATAGACAATTAAGTATCAATTAATCTA 477
 Db 174 CCACCTGGCTGAGTTGCGCTTTCAGCCTATACCGGCTGGCAGCCAGTCCACAGCA 233
 QY 478 CTAACATTTTTTTAGTCTCTGTTTCTATGCGCACGTGCTTCCCATGTTGATTTAGT 537

Db 234 CCAATATCTTCTTCTCCCCAGTGAGCATCGCTACAGCCTTTGCAATGCTCTCCCTGGGA 293
 QY 538 CTAAGCCGATACCCATGACGAGATTTTGAAGGTTTAACTTTTAATTTTACCAGAAATCC 597
 Db 294 CCAAGGCTGACACTCAGGATGAATCTGGAGGCGCTGAATTTTCAACCTCACGGAGATTC 353
 QY 598 CAGAAGCCCAATTCACGAGGGTTTTCAAGAGTTGTGAGAACTTTTGAATCAACCTGATT 657
 Db 354 CGGAGGCTCAGATCCATGAAGGCTTCCAGAACTCTCCGTACCCCTCAACCCAGCCAGACA 413
 QY 658 CTCAATTTGCAATTAACCTACTGTTAAGGTTTATTTTGTCTGAAGTTTAAAAATTTGGTTG 717
 Db 414 GCACGCTCCAGCTGACCCCGCAATGGGCTGTCTCAGCGAGGCGCTCAAGCTAGTGG 473
 QY 718 ACAATTTCTAGAAAGACGCTCAAGAACTATATCATAGTAGGGCTTTTACCGTTAAATTTTG 777
 Db 474 ATAAGTTTTTGGAGGATGTTAAAGCTTGTACCACTCAGAAAGCTTCACTGTCAACTTCG 533
 QY 778 GTGATCTAGGAGGCTAAAGCAATTAAGTATTTTGTGAGAAAGGACCCAGGTTA 837
 Db 534 GGACACCCGAAGAGGCCAAGAAACAGATCAAGGATTTACGTGGAGAGGTTACTCAAGGA 593
 QY 838 AGATCGTTGACCTAGTTAAAGAAATAGATCGTGATACCGCTTCCGACCTAGTTAACTATA 897
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 QY 898 TTTTTCAGAGGTAAAGTGGGAACGCTCTTTTCGAGGTTAAAGATCTACTGAAGAGGAGATT 957
 Db 654 TCTTCTTTAAAGGCAATGGGAGAGACCCCTTTTGAAGTCAAGGACACCCGAGGAGGAGT 713
 QY 958 TTTATCTTTCATCACTACTACTGTCAAAGTTTCCCAATGATGAAAAGACTGGGTATGTCA 1017
 Db 714 TCACGTGGACGAGGTGACCCGCGTGAAGGCTGCTATGATGAAGGCTTTAGGCATGTTA 773
 QY 1018 ATATTCAACATTGCAAAAAATTAAGTTCTTGGTCTTATTAATGAAGTATTTAGGTAACG 1077
 Db 774 ACATCCAGCACTGTAAGAGCTGTTCCAGCTGGGTGCTGCTGATGAATACCTGGGCAATG 833
 QY 1078 CTACTGCTAT-TTTTTTTTACCAGAGGTAAGCTTCAACATTTTAGAGAAATGAGTTG 1136
 Db 834 CCACCGCCATCTCTCTTCNTGGCTGATGAGGGGAAACTACAGGCCTGGAATAATCAATC 893
 QY 1137 ACTCATGACATTATTACTAAATTTTATAGAA 1168
 Db 894 AC-CAGATATCATCAAGGTTCTCTGGAAAA 924

RESULT 9
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 LOCUS AGENCOURT_8492569 NIH_MGC_100 Homo sapiens cDNA clone IMAGE:6296341
 DEFINITION 5', mRNA sequence.
 ACCESSION BQ646142
 VERSION BQ646142.1 GI:21770314
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 982)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: CGAP (Stanford)
 cDNA Library Preparation: Rubin Laboratory
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLCM2504 row: a column: 14

Mon Dec 9 12:50:53 2002

FEATURES
source High quality sequence stop: 647.
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/db_xref="taxon:9606"
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/lab_host="DH10B (phage-resistant)"
/note="Organ: liver; Vector: pOTB7; Site:1: XhoI; Site:2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Size-selected >500bp for average insert size of 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

BASE COUNT 267 a 259 c 238 g 217 t 1 others
ORIGIN
Query Match 18.7%; Score 285.2; DB 14; Length 982;
Best Local Similarity 59.8%; Pred. No. 7.6e-63;
Matches 496; Conservative 0; Mismatches 333; Indels 1; Gaps 1;
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Db 1 GAACCTCCCGTACCTCAACAGCGCCAGCAGCCAGCTCCAGCTGACACCGCGAATGGC 60
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Db 121 TACCACCTCAGAAAGCTTCACTGTCACTTCGCGGACACGAGCGCAAGAAACAGATC 180
QY 807 AATGATTATGTTGAGAAAGGACCCAGGTAAGATCGTTTGACCTAGTTTAAAGAATTTAG 866
Db 181 AAGATTAGCTGAGAGAGGTTACTCAAGGAAATTTGGATTGTTGTTCAAGAGGCTTAC 240
QY 867 CGTGATACCGCTTCGCACTAGTTAACTATATTTTTTTCAGGGTAAAGTGGGAAGCTCT 926
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QY 927 TTGAGGTTTAAAGATCACTCAAGAGGAAGATTTTCATGTTGATCAAGTTACTACTCAAA 986
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Db 361 GTCCCTATGATGAAGGTTTAGGCATGTTTAAATCCAGCACTGTAAGAAGCTGTCCAGC 420
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QY 1346 CTTAACTATTGATGAAAGGGTACCGAGCGCCGCGGTATGTTCTTCTGGAAGCTATTCC 1405
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QY 1406 AATGAGCATTCACCAGAAAGTTAAATTTAATAAACCATTCGTTTCTCTGA 1455
Db 781 CATGTCTATCCCCCGGAGGCGAGTTCAACCAACCCCTTTGTCTCTTA 830
RESULT 10
BQ958958
LOCUS
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AGENCY AGENT 10034701 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:6483305
5', mRNA sequence.
ACCESSION BQ958958
VERSION BQ958958.1 GI:22374436
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 924)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: DCTD/DTF
CDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2667 row: k column: 18
High quality sequence stop: 586.
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/clone="IMAGE:6483305"
/clone_lib="NIH_MGC_40"
/tissue_type="carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: prostate; Vector: pOTB7; Site:1: XhoI; Site:2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

BASE COUNT 251 a 253 c 226 g 193 t 1 others
ORIGIN
Query Match 18.6%; Score 283.8; DB 14; Length 924;
Best Local Similarity 58.4%; Pred. No. 1.7e-62;
Matches 513; Conservative 0; Mismatches 363; Indels 2; Gaps 1;
QY 408 AAAATTAATCTCCAAATTTAGCCGAATTTGCTTTTCTTTGATATAGACAATAGCTATCAA 467
Db 2 AAGATCAACCCCAACCTGGCTGAGTTGCTTTCAGCTATATACCCGCGAGCTGGCACACGAG 61
QY 468 AGTAATTTACTACATTTTTTTTAGTCTCTTATTCCTATTCCTGCTGCTGCTGCTGCTG 527
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Db 302 AAGCTAGTGATAGTTTGGAGGATGTTAAAGAGTTGTACCACTCAGAGCCCTTCACT 361
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Qy 1128 AATGAGTTGACATCATGACATTAATAAATTTTACAGAGAGGATCGTCTAGCG 1185
Db 722 AATGAACACCCAGCATATCATCNACAGTTCCCTGGGAAATGAAGACAGAAAGCTG 781
Qy 1186 CTTCTCTGCACCTGCCAAAGTTAAGTATCACCGGTACTTACGACTTAAATCTGTTTAG 1245
Db 782 CCACCTTACATTTACCCAACTGTCCATTTACTGGAACATGATGCTGAAGAGCGTCTG 841
Qy 1246 GCAGTGTAGTATTACCAAGTTTTTCTACGGTGCC 1283
Db 842 GTCAACTGGGCATCACTAAGGTCTTCAGCAATGGGGC 879

RESULT 11
BM924813
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  1194 bp mRNA linear EST 12-MAR-2002
  AGENCOURT_6653921 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5761267
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ACCESSION
  BM924813
VERSION
  BM924813.1 GI:19375192
KEYWORDS
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SOURCE
  human.
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  NIH-MGC http://mgi.nci.nih.gov/
  National Institutes of Health, Mammalian Gene Collection (MGC)
  Unpublished (1999)
  Contact: Robert Strausberg, Ph.D.
  Email: cgapbs-remail.nih.gov
  Tissue Procurement: Life Technologies, Inc.
  cDNA Library Preparation: Life Technologies, Inc.
  cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
  DNA Sequencing by: Agencourt Bioscience Corporation
  Clone distribution: MGC clone distribution information can be
  found through the I.M.A.G.E. Consortium/LLNL at:
  http://image.llnl.gov
  Plate: LLAM12809 row: J column: 20
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High quality sequence stop: 662.
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  /note="Organ: pooled colon, kidney, stomach; Vector:
  pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
  source anonymous pool of 3 colons, age 26 yo male, 49 yo
  female, 71 yo male colon; 46 yo male kidney, and pool of 2
  stomachs, 62 yo male and 70 yo female. Library is
  oligo-dr primed and directionally cloned (EcoRV site is
  destroyed upon cloning). Average insert size 1.4 kb,
  insert size range 1-3 kb. Library is normalized and
  enriched for full-length clones and was constructed by C.
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  023. Note: this is a NIH_MGC Library."
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ORIGIN
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Best Local Similarity 61.2%; Pred. No. 4e-60;
Matches 444; Conservative 0; Mismatches 282; Indels 0; Gaps 0;

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Qy 832 AGGGTAAGATCGTTCACCTAGTTAAAGAAATTAAGATCGTGATACCGTCTTCGCACCTAGTTA 891
Db 67 AAGGAAATTTGGTCAAGAGCTTGACAGAGACACAGTTTTTGTCTGTGTGA 126
Qy 892 ACTATATTTTTTCAAGGGTAAGTGGGAACGTCCTTTTCGAGGTTAAAGATACTGAAGAGG 951
Db 127 ATTACATCTCTTTAAAGGCAATGGGAGAGACCCCTTTGAAGTCAAGACACCGAGGAAG 186
Qy 952 AGATTTTCATGTTGATCAAGTTACTACTGTCAAGTTTCAATGATGAAAGACTGGGTA 1011
Db 187 AGGACTTCCAGCTGGACGAGGTGACACCGGTGAAGGTGCCTATGATGAACGTTTAGGCA 246
Qy 1012 TGTTCAATATTCACATTCGCAAAAATTAAGTTCTTGGGCTTATTATTAATCAAGTATTAG 1071
Db 247 TGTTTAACATCCAGCATCTGAAGAGCTGTCCAGCTGGTGTCTGTGATGAATACCTCG 306
Qy 1072 GTAACGCTACTGCTATTTTTTTTTTACAGACGAAGGTAAAGCTTCAACATTTAGAGAAATG 1131
Db 307 GCAATGCCACCGCCATCTTCTCCTGCTGATGAGGGGAAACTACAGCACCTCGAAAGATG 366
Qy 1132 AGTTGACATCATGACATTAATAATTTTAGAGACGAGGATCGTCTAGCGCTTCTC 1191
Db 367 AACTCACCACGATATCATCAACCAAGTTCTGGAATAATGAAGACAGAAGGTCTGCCAGCT 426
Qy 1192 TGCACCTGCCAAAGTTAAGTATCACCGGTACTTACGACTTAAAAATCTGTTTAGGCCAGT 1251
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Db 547 CCCTGAAGCTCTCCAAAGCGCTGATGAAGCTGTGTGACCATCGACAGAAAGGACTG 606
Qy 1372 AGGCGCGCGCGCTATGTTCTCTGGAAGCTATTCCAATGAGCATTTCCACCAGAGTTTAAAT 1431
Db 607 AAGCTGTGGGGCCATGTTTTTAGAGGCCATACCCATGCTATCCCCCGGAGGTCAGT 666
Qy 1432 TTATAAACCATCTGTTTTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1491
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/db_xref="taxon:9606"
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Db 187 ATTGTGGATTGGTCAAGGAGCTTGACAGAGACACAGTTTTTCTCTGGTGAATTACATC 246

sflii (ggccgctggcc): Site 2: sflii (ggccattatggcc): 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTAATGCCC-3', and 3' adaptor sequence: 5'-ATTCTAGAGCGCGGCGGACATG-dt(30)BN-3' (where B = A, C, G, or T). Average insert size 1.85 kb (range 1.0-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH-MGC Library.*

BASE COUNT 222 a 215 c 191 g 166 t
ORIGIN

Query Match 17.6%; Score 268; DB 12; Length 796;
Best Local Similarity 60.0%; Pred. No. 2e-58;
Matches 479; Conservative 0; Mismatches 317; Indels 2; Gaps 2;

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QY 439 TTTCTTTGTATAGACAATAGCTCATCAAAAGTAATTTCTACTACATTTTCTTTAGTCCCTG 498
DB 61 TCAGCCTATACCGCCAGCTGGCACACCCAGTCCACACAGCACCAATATCTTCTTCCCCAG 120
QY 499 TTTCTATGCGCCTGCTTTCGCCATGTTGAGTTAGTACTAAAGCGGATACCCCATGACG 558
DB 121 TGAGCATCGGTACAGCCTTTGCAATGCTCTCCCTGGGGACCAAGGCTGACACTCAGATG 180
QY 559 AGATTTTAGAAGGTTTAAACCTTTAAATTTGACCGAAATFCCAGAAAGCCCAATTCACAGG 618
DB 181 AATCTCTGGAGGCTGAATTTCAACCTCAGGAGATTCGGAGGCTCAGATCCATGAAG 240
QY 619 GTTTTCAAGAGTGTGAGAACTTTGAATCAACTGATTTCTCAATTCGAATTAATTAAGT 678
DB 241 GCTTCCAGGAACCTCTCCATACCTCAACAGCCAGACAGCCAGCTCCAGCTGACCAACG 300
QY 679 GTAACGGTTTATTTTGTCTGAAGGTTTAAATTTGGTTGACAAATTCCTAGAGACGTCA 738
DB 301 GCAATGGCTGTTCTCTCAGCAGGCGCTGAAGCTAGTGGATAAGTTTNTGGAGATGTTA 360
QY 739 AGAACTATATCAVATGAGGCTTTTACCGTTAAATTTTGGTGATCTAGGAAAGCTAAA 798
DB 361 AAAAGTTGTACCACTCAGAAGCCTTCACTGTCAACTTCGGGGACACCCGAGAGGCGCAAGA 420
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DB 480 AGCTTGACAGAGACACAGTTTTCCTCTGTTGTAATTAATCTCTTTAAAGGCAATGGG 539
QY 919 AACGTCCTTCGAGGTTAAGATCTGAAGAGGAAGATTTTCATGCTTCATCAAGTTACTA 978
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DB 720 CTGATGAGGGAAATTTACAGCACCTGGGAACATGAATCAACCCA-GATATCATCACCAAGT 778
QY 1159 TTTTAGAGAACGAGGATC 1176
DB 779 TCTTGGAACACTGAGACC 796

QY 810 GATTATGTTGAGAAGGACCCAGGTAAGATCGTTGACCTAGTTAAAGAAATAGATCGT 869
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ACCESSION BG567260
VERSION BG567260.1 GI:13574913
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SOURCE human.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 796)
NIH-MGC <http://mgi.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cyabs@remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
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FEATURES
source

Mon Dec 9 12:50:53 2002

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Job time : 1545.5 secs
